

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo
- (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-162
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684
- (x) Note: In all the amino acid sequences below, "Xaa"
stands for one of the three stop codons.

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2529 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCTCAGGT	CGGCGTCGTA	CCAGCCGCTG	AAGCGGTTCT	CCAGGTTCCA	GGCGCTCTCG	60
CCATGCCGGA	TCAGCACCAG	CTTGTAGCTC	GTGCCGAATT	CGGCACGAGG	TTGCTTTGGG	120
AATGAGCAAG	GTCAAAACTG	CTCTGCACTC	ACAGACAACA	CTGAAGGGAA	GACACTGGCT	180
TCAGTAGTGA	AGGCTTCAGT	TTTTCGCCAG	CTAGGTGTAA	ACTGGGACAT	AGAGTGCTGG	240
ATGAAAGGGG	ACTTGACATT	ATTCATCTGT	CATATGGAGC	CATTACCTAA	GAACCCCTTC	300
AAGAATTATG	ACTCTAAGGT	CCATCTTTTA	TATGATCTGC	CTGAAGTCAT	AGATGATTCTG	360
CCTCTGCCCC	CACTGAAAGA	CAGCTTTCAG	ACTGTCCAAT	GCAACTGCAG	TCTTCGGGGA	420
TGTGAATGTC	ATGTGCCGGT	ACCCAGAGCC	AAACTCAACT	ACGCTCTTCT	GATGTATTTG	480
GAAATCACAT	CTGCCGGTGT	GAGTTTTTCT	TCACCTCTGA	TGTCACCTGCA	GCCCATGCTT	540
GTTGTGAAAC	CCGATCCACC	CTTAGGTTTG	CATATGGAAG	TCACAGATGA	TGGTAATTTA	600
AAGATTTCTT	GGGACAGCCA	AACAATGGCA	CCATTTCCGC	TTCAATATCA	GGTGAAATAT	660
TTAGAGAATT	CTACAATTGT	AAGAGAGGCT	GCTGAAATTG	TCTCAGCTAC	ATCTCTGCTG	720
GTAGACAGTG	TGCTTCCTGG	ATCTTCATAT	GAGGTCCAGG	TGAGGAGCAA	GAGACTGGAT	780
GGTTCAGGAG	TCTGGAGTGA	CTGGAGTTCA	CCTCAAGTCT	TTACCACACA	AGATGTTGTG	840
TATTTTCCAC	CCAAAATTCT	GACTAGTGTT	GGATCGAATG	CTTCTTTTCA	TTGCATCTAC	900
AAAAACGAAA	ACCAGATTAT	CTCCTCAAAA	CAGATAGTTT	GGTGGAGGAA	TCTAGCTGAG	960
AAAATCCCTG	AGATACAGTA	CAGCATTGTG	AGTGACCGAG	TTAGCAAAGT	TACCTTCTCC	1020
AACCTGAAAG	CCACCAGACC	TCGAGGGAAG	TTTACCTATG	ACGCAGTGTA	CTGCTGCAAT	1080
GAGCAGGCGT	GCCATCACCG	CTATGCTGAA	TTATACGTGA	TCGATGTCAA	TATCAATATA	1140
TCATGTGAAA	CTGACGGGTA	CTTAACATAA	ATGACTTGCA	GATGGTCACC	CAGCACAATC	1200
CAATCACTAG	TGGGAAGCAC	TGTGCAGCTG	AGGTATCACA	GGCGCAGCCT	GTATTGTCCT	1260
GATAGTCCAT	CTATTCATCC	TACGTCTGAG	CCCAAAACT	GCGTCTTACA	GAGAGACGGC	1320
TTTTATGAAT	GTGTTTTCCA	GCCAATCTTT	CTATTATCTG	GCTATACAAT	GTGGATCAGG	1380
ATCAACCATT	CTTTAGGTTC	ACTTGACTCG	CCACCAACGT	GTGTCCTTCC	TGACTCCGTA	1440
GTAAAACCAC	TACCTCCATC	TAACGTAAAA	GCAGAGATTA	CTGTAAACAC	TGGATTATTG	1500
AAAGTATCTT	GGGAAAAGCC	AGTCTTTCCG	GAGAATAACC	TTCAATTCCA	GATTCGATAT	1560
GGCTTAAGTG	GAAAAGAAAT	ACAATGGAAG	ACACATGAGG	TATTCGATGC	AAAGTCAAAG	1620
TCTGCCAGCC	TGCTGGTGTC	AGACCTCTGT	GCAGTCTATG	TGGTCCAGGT	TCGCTGCCGG	1680
CGGTTGGATG	GACTAGGATA	TTGGAGTAAT	TGGAGCAGTC	CAGCCTATAC	GCTTGTCATG	1740
GATGTAAAAG	TTCTATGAG	AGGGCCTGAA	TTTTGGAGAA	AAATGGATGG	GGACGTTACT	1800
AAAAAGGAGA	GAAATGTCAC	CTTGCTTTGG	AAGCCCCTGA	CGAAAAATGA	CTCACTGTGT	1860
AGTGTGAGGA	GGTACGTGGT	GAAGCATCGT	ACTGCCACAC	ATGGGACGTG	GTCAGAAGAT	1920

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GTGGGAAATC GGACCAATCT CACTTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT 1980
CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTTTA ACCTTACCTT CTCATGGCCC 2040
ATGAGTAAAG TGAGTGCTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC 2100
ATCCTTTCCT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG 2160
AAGATCCTTA ATGAAGATGA TGGAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG 2220
TTTTATATCC ACGATAATTT TATTCCTATC GAGAAATATC AGTTTAGTCT TTACCCAGTA 2280
TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC 2340
AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTTT CTCTTGTGTC 2400
CTACTGCTCG GAACACTGTT AATTTACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT 2460
GTTCCAAACC CCAAGAATTG TTCCTGGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC 2520
ACTCTTTGA 2529

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Gly Leu Arg Ser Ala Ser Tyr Gln Pro Leu Lys Arg Phe Ser Arg Phe
1           5           10           15
Gln Ala Leu Ser Pro Cys Arg Ile Ser Thr Ser Leu Xaa Leu Val Pro
20           25           30
Asn Ser Ala Arg Gly Cys Phe Gly Asn Glu Gln Gly Gln Asn Cys Ser
35           40           45
Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala Ser Val Val Lys
50           55           60
Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp Ile Glu Cys Trp
65           70           75           80
Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met Glu Pro Leu Pro
85           90           95
Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His Leu Leu Tyr Asp
100          105          110

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Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	Leu	Lys	Asp	Ser		
		115					120					125					
Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	Cys	Glu	Cys	His		
	130					135					140						
Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	Leu	Met	Tyr	Leu		
	145				150					155					160		
Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	Leu	Met	Ser	Leu		
				165					170					175			
Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	Gly	Leu	His	Met		
			180					185					190				
Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	Asp	Ser	Gln	Thr		
		195					200					205					
Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	Leu	Glu	Asn	Ser		
	210					215					220						
Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	Thr	Ser	Leu	Leu		
	225				230					235					240		
Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val	Gln	Val	Arg	Ser		
				245					250					255			
Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp	Ser	Ser	Pro	Gln		
			260					265					270				
Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro	Lys	Ile	Leu	Thr		
		275					280					285					
Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr	Lys	Asn	Glu	Asn		
	290					295					300						
Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg	Asn	Leu	Ala	Glu		
	305				310					315					320		
Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp	Arg	Val	Ser	Lys		
				325					330					335			
Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg	Gly	Lys	Phe	Thr		
			340					345					350				
Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys	His	His	Arg	Tyr		
		355					360					365					
Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile	Ser	Cys	Glu	Thr		
	370					375					380						
Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Pro	Ser	Thr	Ile		
	385				390					395					400		
Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr	His	Arg	Arg	Ser		
				405					410					415			
Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr	Ser	Glu	Pro	Lys		
			420					425					430				
Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys	Val	Phe	Gln	Pro		
		435					440					445					
Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg	Ile	Asn	His	Ser		
	450					455					460						

Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu	Pro	Asp	Ser	Val	465	470	475	480
Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu	Ile	Thr	Val	Asn	485	490	495	
Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val	Phe	Pro	Glu	Asn	500	505	510	
Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly	Lys	Glu	Ile	Gln	515	520	525	
Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys	Ser	Ala	Ser	Leu	530	535	540	
Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln	Val	Arg	Cys	Arg	545	550	555	560
Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser	Ser	Pro	Ala	Tyr	565	570	575	
Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly	Pro	Glu	Phe	Trp	580	585	590	
Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg	Asn	Val	Thr	Leu	595	600	605	
Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg	610	615	620	
Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp	625	630	635	640
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His	645	650	655	
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn	660	665	670	
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu	675	680	685	
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp	690	695	700	
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp	705	710	715	720
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser	725	730	735	
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	740	745	750	
Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	755	760	765	
Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	770	775	780	
Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	785	790	795	800
Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	805	810	815	

Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
820 825 830

Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
835 840

(2) INFORMATION FOR SEQ ID NO:3:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2848 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: A40 (OB-Rb)
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|            |             |             |            |            |            |      |
|------------|-------------|-------------|------------|------------|------------|------|
| CTCATTGAGA | GTGCCAACGG  | GAAGGCTTAA  | TTAACCTTTG | GAANTGAGTC | CGAAGAGTCT | 60   |
| GGAAGTNTGT | AAGATGGAAG  | ATACTATACA  | AGATACTTCA | GAGCTGTACA | TTCTTCCAGG | 120  |
| GATGTAGGCT | AGCAGTTATT  | TCATTAGTAT  | ATGTCTATTT | TAGAATGGGA | AGAATTAGGA | 180  |
| AGATGAATGG | AGCCTGTGTC  | TTTCACTACT  | CTCCCAGGAG | GTTCCAGAAT | AGCNAAGTG  | 240  |
| TCAGCCAGAA | TTCTTGAAGT  | CATAGACTGG  | AGTTAGAGAT | GAACATAAGC | TCATGTTAAG | 300  |
| CCTGGGTTAC | TTCTTATCAT  | CCTTAATTTT  | GAAAGCTAAG | AGGGCCTAAC | CATCAAGAAC | 360  |
| GTCCTGGAGG | AAAGAATGTT  | TTTAACGCCA  | TTATTCAGTC | AAAGAAATTA | AGACTTGAGA | 420  |
| GAAATGCTCA | TTTCTTCTCT  | CATGATGGCT  | CCTTACACCT | TACTTCTACC | GTACGATCCA | 480  |
| TGNGGCCCTA | CCCACGCAGG  | ATACATGCAT  | CTATATGAGA | GTGTCTNCCC | CTTCTAACTC | 540  |
| AGAGACTCTT | GTTCTAGTCT  | GTGNTATAAA  | ATTGAGCTTG | TGGAAGCTTT | CTGAGGGGTT | 600  |
| GGCAGCATTC | AATTTTACCT  | GCAATAGGTA  | AAGGTAATCT | TTTGGAAGT  | GAAGAGTGTT | 660  |
| ATTAGACATT | TCAGAAAGAA  | CAAACAGGAT  | TGGGGCTGCT | ATGTGTTCTA | CACAGGAATC | 720  |
| TTCCATAACA | CAGAATAATT  | TATGTAGATA  | GAGACAAGAT | GGAAATGCCC | AGGGCCCCAA | 780  |
| AATAGCCGCT | GTTATTTGTT  | AACCTTCAAG  | GTTTTCTGTT | TGTTTATCTG | TTTCTTGCGC | 840  |
| AGGATCATCT | TCCAAGCACA  | TCCTGGGGGA  | ACAGTGGCAG | AGTCACTCGA | GTTCATGAAA | 900  |
| CTATGGTGAC | ATCTGAGCTT  | CCTTG GTTCT | TCACAGAACA | TAAGCAGTTC | CTTTGCTTGC | 960  |
| TTGTTAGATG | AGAAAAC TTC | CTTGTCAGTC  | TGTCTCTACG | ACTAGAATGG | AAAGCCTTAC | 1020 |
| TACTTCCTAT | GTATTCTTAA  | TATTTCAAAT  | GTCTTAATTA | TGTTTGGCTT | CTCTGTCTTT | 1080 |
| AAGGGATTTA | GTCTCTGGAT  | TTGAAGAAAT  | AAATAAATAA | ATAAAGGAAA | ACTAATTTTC | 1140 |

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| TCGTGCCGGA | TGACTGCTAG | CTGAGCTCAG | GCCTACTGCA | TTCTACATTT  | CGACTCTCTC | 1200 |
| CCTCTTCCCC | AGTGCTTTAG | CACTGGACTG | GGCAGTNCCT | GGCCTGGTCT  | AACTCCTGTT | 1260 |
| TCCTGGTGGG | AATGTATAAT | AAGAACTCCA | TGAGTTCTGG | TATAAAACACT | GTGGTCTGTG | 1320 |
| TGCTAATTAA | ATCTNGTGTT | TCCTACAGCC | CCTGACGAAA | AATGACTCAC  | TGTGTAGTGT | 1380 |
| GAGGAGGTAC | GTGGTGAAGC | ATCGTACTGC | CCACAATGGG | ACGTGGTCAG  | AAGATGTGGG | 1440 |
| AAATCGGACC | AATCTCACTT | TCCTGTGGAC | AGAACCAGCG | CACACTGTTA  | CAGTTCTGGC | 1500 |
| TGTCAATTCC | CTCGGCGCTT | CCCTTGTGAA | TTTTAACCTT | ACCTTCTCAT  | GGCCCATGAG | 1560 |
| TAAAGTGAGT | GCTGTGGAGT | CACTCAGTGC | TTATCCCCTG | AGCAGCAGCT  | GTGTCATCCT | 1620 |
| TTCTTGACA  | CTGTCACCTG | ATGATTATAG | TCTGTTATAT | CTGGTTATTG  | AATGGAAGAT | 1680 |
| CCTTAATGAA | GATGATGGAA | TGAAGTGGCT | TAGAATTCCC | TCGAATGTTA  | AAAAGTTTTA | 1740 |
| TATCCACGAT | AATTTTATTC | CCATCGAGAA | ATATCAGTTT | AGTCTTTACC  | CAGTATTTAT | 1800 |
| GGAAGGAGTT | GGAAAACCAA | AGATAATTAA | TGGTTTCACC | AAAGATGCTA  | TCGACAAGCA | 1860 |
| GCAGAATGAC | GCAGGGCTGT | ATGTCATTGT | ACCCATAATT | ATTTCTCTCT  | GTGTCCTACT | 1920 |
| GCTCGGAACA | CTGTTAATTT | CACACCAGAG | AATGAAAAAG | TTGTTTTGGG  | ACGATGTTCC | 1980 |
| AAACCCCAAG | AATTGTTTCT | GGGCACAAGG | ACTGAATTTT | CAAAAGCCTG  | AAACATTNGA | 2040 |
| GCATCTTTTT | ACCAAGCATG | CAGAATCAGT | GATATTTGGT | CCTCTTCTTC  | TGGAGCCTGA | 2100 |
| ACCCATTTCA | GAAGAAATCA | GTGTCGATAC | AGCTTGGAAG | AATAAAGATG  | AGATGGTCCC | 2160 |
| AGCAGCTATG | GTCTCCCTNC | TNNGGACCAC | ACCAGACCCT | GAAAGCAGTT  | CTATTTGTNT | 2220 |
| TAGTGACCAG | TGTAACAGTG | CTAACTTCTC | TGGGTCTCAG | AGCACCCAGG  | TAACCTGTGA | 2280 |
| GGATGAGTGT | CAGAGACAAC | CCTCAGTTAA | ATATGCAACT | CTGGTCAGCA  | ACGATAAACT | 2340 |
| AGTGGAAGCT | GATGAAGAGC | AAGGGTTTAT | CCATAGTCCT | GTCAGCAACT  | GCATCTCCAG | 2400 |
| TAATCATTCC | CCACTGAGGC | AGTCTTTCTC | TAGCAGCTCC | TGGGAGACAG  | AGGCCAGAC  | 2460 |
| ATTTTTCTCT | TTATCAGACC | AGCAACCCAC | CATGATTTCA | CCACAACCTT  | CATTCTCGGG | 2520 |
| GTTGGATGAG | CTTTTGGAAC | TGGAGGGAAG | TTTTCTTGAA | GAAAATCACA  | GGGAGNAGTC | 2580 |
| TGTCTGTTAT | CTAGGAGTCA | CCTCCGTCCN | CAGAAGAGAG | AGTGGTGTGC  | TTTTGACTGG | 2640 |
| TGAGGCAGGA | ATCCTGTGCA | CATTCCCAGC | CCAGTGTCTG | TTCAGTGACA  | TCAGGATCCT | 2700 |
| CCAGGAGAGA | TGCTCACACT | TTGTAGAAAA | TAATTTGAGT | TTAGGGACCT  | CTGGTGAGAA | 2760 |
| CTTTGGTCTT | AACATGCCCC | AATTCCAAAC | CTGTTCCACG | CACAGTCACA  | AGATAATGGA | 2820 |
| GAATAAGATG | TGTGACTTAA | CTGTGTAA   |            |             |            | 2848 |

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Asp | Leu | Val | Ser | Gly | Phe | Glu | Glu | Ile | Asn | Lys | Ile | Lys | Glu | 1   | 5   | 10  | 15  |
| Asn | Phe | Ser | Arg | Ala | Gly | Leu | Leu | Ala | Glu | Leu | Arg | Pro | Thr | Ala | Phe | 20  | 25  | 30  |     |
| Tyr | Ile | Ser | Thr | Leu | Ser | Leu | Phe | Pro | Ser | Ala | Leu | Ala | Leu | Asp | Trp | 35  | 40  | 45  |     |
| Ala | Val | Pro | Gly | Leu | Val | Leu | Leu | Phe | Pro | Gly | Gly | Asn | Val | Glu | Leu | 50  | 55  | 60  |     |
| His | Glu | Phe | Trp | Tyr | Lys | His | Cys | Gly | Leu | Cys | Ala | Asn | Ile | Xaa | Cys | 65  | 70  | 75  | 80  |
| Phe | Leu | Gln | Pro | Leu | Thr | Lys | Asn | Asp | Ser | Leu | Cys | Ser | Val | Arg | Arg | 85  | 90  | 95  |     |
| Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | Asn | Gly | Thr | Trp | Ser | Glu | Asp | 100 | 105 | 110 |     |
| Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | Leu | Trp | Thr | Glu | Pro | Ala | His | 115 | 120 | 125 |     |
| Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | Leu | Gly | Ala | Ser | Leu | Val | Asn | 130 | 135 | 140 |     |
| Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | Ser | Lys | Val | Ser | Ala | Val | Glu | 145 | 150 | 155 | 160 |
| Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | Ser | Cys | Val | Ile | Leu | Ser | Trp | 165 | 170 | 175 |     |
| Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | Leu | Tyr | Leu | Val | Ile | Glu | Trp | 180 | 185 | 190 |     |
| Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | Lys | Trp | Leu | Arg | Ile | Pro | Ser | 195 | 200 | 205 |     |
| Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Asp | Asn | Phe | Ile | Pro | Ile | Glu | Lys | 210 | 215 | 220 |     |
| Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Val | Phe | Met | Glu | Gly | Val | Gly | Lys | Pro | 225 | 230 | 235 | 240 |
| Lys | Ile | Ile | Asn | Gly | Phe | Thr | Lys | Asp | Ala | Ile | Asp | Lys | Gln | Gln | Asn | 245 | 250 | 255 |     |
| Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | Ile | Ile | Ile | Ser | Ser | Cys | Val | 260 | 265 | 270 |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | His | Gln | Arg | Met | Lys | Lys | Leu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | Asn | Cys | Ser | Trp | Ala | Gln | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Asn | Phe | Gln | Lys | Pro | Glu | Thr | Phe | Glu | Gln | Leu | Phe | Thr | Lys | His |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Glu | Ser | Val | Ile | Phe | Gly | Pro | Leu | Leu | Leu | Glu | Pro | Glu | Pro | Ile |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Glu | Glu | Ile | Ser | Val | Asp | Thr | Ala | Trp | Lys | Asn | Lys | Asp | Glu | Met |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Pro | Ala | Ala | Met | Val | Ser | Leu | Leu | Trp | Thr | Thr | Pro | Asp | Pro | Glu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Ser | Ser | Ile | Cys | Ile | Ser | Asp | Gln | Cys | Asn | Ser | Ala | Asn | Phe | Ser |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Gly | Ser | Gln | Ser | Thr | Gln | Val | Cys | Glu | Asp | Glu | Cys | Gln | Arg | Gln | Pro |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ser | Val | Lys | Tyr | Ala | Thr | Leu | Val | Ser | Asn | Asp | Lys | Leu | Val | Glu | Thr |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | Glu | Glu | Gln | Gly | Phe | Ile | His | Ser | Pro | Val | Ser | Asn | Cys | Ile | Ser |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ser | Asn | His | Ser | Pro | Leu | Arg | Gln | Ser | Phe | Ser | Ser | Ser | Ser | Trp | Glu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Thr | Glu | Ala | Gln | Thr | Phe | Phe | Leu | Leu | Ser | Asp | Gln | Gln | Pro | Thr | Met |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ile | Ser | Pro | Gln | Leu | Ser | Phe | Ser | Gly | Leu | Asp | Glu | Leu | Leu | Glu | Leu |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Glu | Gly | Ser | Phe | Pro | Glu | Glu | Asn | His | Arg | Glu | Lys | Ser | Val | Cys | Tyr |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Leu | Gly | Val | Thr | Ser | Val | Asn | Arg | Arg | Glu | Ser | Gly | Val | Leu | Leu | Thr |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Gly | Glu | Ala | Gly | Ile | Leu | Cys | Thr | Phe | Pro | Ala | Gln | Cys | Leu | Phe | Ser |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Asp | Ile | Arg | Ile | Leu | Gln | Glu | Arg | Cys | Ser | His | Phe | Val | Glu | Asn | Asn |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Leu | Ser | Leu | Gly | Thr | Ser | Gly | Glu | Asn | Phe | Gly | Pro | Tyr | Met | Pro | Gln |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Phe | Gln | Thr | Cys | Ser | Thr | His | Ser | His | Lys | Ile | Met | Glu | Asn | Lys | Met |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Cys | Asp | Phe | Thr | Val |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 580 |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 961 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT  | 60  |
| TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT  | 120 |
| CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT  | 180 |
| GTTTCCTGGT GGGAAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT | 240 |
| GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG  | 300 |
| TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT  | 360 |
| GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT  | 420 |
| GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT  | 480 |
| GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT  | 540 |
| CCTTTCCTGG ACACTGTCAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA  | 600 |
| GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT  | 660 |
| TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT  | 720 |
| TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA  | 780 |
| GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTTCCT CTTGTGTCCT | 840 |
| ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT  | 900 |
| TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA  | 960 |
| A                                                                  | 961 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 319 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Leu | Arg | Asp | Leu | Val | Ser | Gly | Phe | Glu | Glu | Ile | Asn | Lys | Xaa | Ile | Lys | 1   | 5   | 10  | 15 |
| Glu | Asn | Xaa | Phe | Ser | Arg | Ala | Gly | Xaa | Leu | Leu | Ala | Glu | Leu | Arg | Pro | 20  | 25  | 30  |    |
| Thr | Ala | Phe | Tyr | Ile | Ser | Thr | Leu | Ser | Leu | Phe | Pro | Ser | Ala | Leu | Ala | 35  | 40  | 45  |    |
| Leu | Asp | Trp | Ala | Val | Pro | Gly | Leu | Val | Xaa | Leu | Leu | Phe | Pro | Gly | Gly | 50  | 55  | 60  |    |
| Asn | Val | Xaa | Xaa | Glu | Leu | His | Glu | Phe | Trp | Tyr | Lys | His | Cys | Gly | Leu | 65  | 70  | 75  |    |
| Cys | Ala | Asn | Xaa | Ile | Xaa | Cys | Phe | Leu | Gln | Pro | Leu | Thr | Lys | Asn | Asp | 85  | 90  | 95  |    |
| Ser | Leu | Cys | Ser | Val | Arg | Arg | Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | 100 | 105 | 110 |    |
| Asn | Gly | Thr | Trp | Ser | Glu | Asp | Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | 115 | 120 | 125 |    |
| Leu | Trp | Thr | Glu | Pro | Ala | His | Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | 130 | 135 | 140 |    |
| Leu | Gly | Ala | Ser | Leu | Val | Asn | Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | 145 | 150 | 155 |    |
| Ser | Lys | Val | Ser | Ala | Val | Glu | Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | 165 | 170 | 175 |    |
| Ser | Cys | Val | Ile | Leu | Ser | Trp | Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | 180 | 185 | 190 |    |
| Leu | Tyr | Leu | Val | Ile | Glu | Trp | Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | 195 | 200 | 205 |    |
| Lys | Trp | Leu | Arg | Ile | Pro | Ser | Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Asp | 210 | 215 | 220 |    |
| Asn | Phe | Ile | Pro | Ile | Glu | Lys | Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Val | Phe | 225 | 230 | 235 |    |
| Met | Glu | Gly | Val | Gly | Lys | Pro | Lys | Ile | Ile | Asn | Gly | Phe | Thr | Lys | Asp | 245 | 250 | 255 |    |
| Ala | Ile | Asp | Lys | Gln | Gln | Asn | Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | 260 | 265 | 270 |    |
| Ile | Ile | Ile | Ser | Ser | Cys | Val | Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | 275 | 280 | 285 |    |
| His | Gln | Arg | Met | Lys | Lys | Leu | Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | 290 | 295 | 300 |    |
| Asn | Cys | Ser | Trp | Ala | Gln | Gly | Leu | Asn | Phe | Gln | Lys | Val | Thr | Val |     |     |     |     |    |

305

310

315

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A8 (OB-Rd)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT | 60   |
| GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG | 120  |
| AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG | 180  |
| AAGGGGGCTT CTGAAGCAAT TGTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCCCT | 240  |
| GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AACTGCTCT  | 300  |
| GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT | 360  |
| CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC | 420  |
| ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT | 480  |
| CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTCGCCTC TGCCCCCACT GAAAGACAGC | 540  |
| TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC | 600  |
| AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT | 660  |
| TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTTG TGAAACCCGA TCCACCCTTA | 720  |
| GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTTGGGA CAGCCAAACA | 780  |
| ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA | 840  |
| GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT | 900  |
| TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG | 960  |
| AGTTCACCTC AAGTCTTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT | 1020 |
| AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAA ACGAAAACCA GATTATCTCC   | 1080 |
| TCAAAACAGA TAGTTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC | 1140 |
| ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA | 1200 |
| GGGAAGTTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT | 1260 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| GCTGAATTAT | ACGTGATCGA | TGTCAATATC | AATATATCAT | GTGAAACTGA | CGGGTACTTA | 1320 |
| ACTAAAATGA | CTTGCAGATG | GTCACCCAGC | ACAATCCAAT | CACTAGTGGG | AAGCACTGTG | 1380 |
| CAGCTGAGGT | ATCACAGGCG | CAGCCTGTAT | TGTCCTGATA | GTCCATCTAT | TCATCCTACG | 1440 |
| TCTGAGCCCA | AAAACTGCGT | CTTACAGAGA | GACGGCTTTT | ATGAATGTGT | TTTCCAGCCA | 1500 |
| ATCTTTCTAT | TATCTGGCTA | TACAATGTGG | ATCAGGATCA | ACCATTCTTT | AGGTTCACTT | 1560 |
| GACTCGCCAC | CAACGTGTGT | CCTTCCTGAC | TCCGTAGTAA | AACCACTACC | TCCATCTAAC | 1620 |
| GTAAAAGCAG | AGATTACTGT | AAACACTGGA | TTATTGAAAG | TATCTTGGA  | AAAGCCAGTC | 1680 |
| TTTCCGGAGA | ATAACCTTCA | ATTCCAGATT | CGATATGGCT | TAAGTGAAA  | AGAAATACAA | 1740 |
| TGGAAGACAC | ATGAGGTATT | CGATGCAAAG | TCAAAGTCTG | CCAGCCTGCT | GGTGTGAGAC | 1800 |
| CTCTGTGCAG | TCTATGTGGT | CCAGGTTTCG | TGCCGGCGGT | TGGATGGACT | AGGATATTGG | 1860 |
| AGTAATTGGA | GCAGTCCAGC | CTATACGCTT | GTCATGGATG | TAAAAGTTCC | TATGAGAGGG | 1920 |
| CCTGAATTTT | GGAGAAAAAT | GGATGGGGAC | GTTACTAAAA | AGGAGAGAAA | TGTCACCTTG | 1980 |
| CTTTGGAAGC | CCCTGACGAA | AAATGACTCA | CTGTGTAGTG | TGAGGAGGTA | CGTGGTGAAG | 2040 |
| CATCGTACTG | CCCACAATGG | GACGTGGTCA | GAAGATGTGG | GAAATCGGAC | CAATCTCACT | 2100 |
| TTCCTGTGGA | CAGAACCAGC | GCACACTGTT | ACAGTTCTGG | CTGTCAATTC | CCTCGGCGCT | 2160 |
| TCCCTTGTA  | ATTTTAACCT | TACCTTCTCA | TGGCCCATGA | GTAAAGTGAG | TGCTGTGGAG | 2220 |
| TCACTCAGTG | CTTATCCCCT | GAGCAGCAGC | TGTGTCATCC | TTTCCTGGAC | ACTGTCACCT | 2280 |
| GATGATTATA | GTCTGTTATA | TCTGGTTATT | GAATGGAAGA | TCCTTAATGA | AGATGATGGA | 2340 |
| ATGAAGTGGC | TTAGAATTCC | CTCGAATGTT | AAAAAGTTTT | ATATCCACGA | TAATTTTATT | 2400 |
| CCCATCGAGA | AATATCAGTT | TAGTCTTTAC | CCAGTATTTA | TGGAAGGAGT | TGGAACCA   | 2460 |
| AAGATAATTA | ATGGTTTCAC | CAAAGATGCT | ATCGACAAGC | AGCAGAATGA | CGCAGGGCTG | 2520 |
| TATGTCATTG | TACCCATAAT | TATTTCTCT  | TGTGTCCTAC | TGCTCGGAAC | ACTGTTAATT | 2580 |
| TCACACCAGA | GAATGAAAAA | GTTGTTTTGG | GACGATGTTT | CAAACCCCAA | GAATTGTTCC | 2640 |
| TGGGCACAAG | GACTGAATTT | CCAAAAGGAT | ATATCTTTAC | ATGAAGTTTT | TATTTTCAGA | 2700 |
| TAG        |            |            |            |            |            | 2703 |

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Cys | Gln | Lys | Phe | Tyr | Val | Val | Leu | Leu | His | Trp | Glu | Phe | Leu | 1   | 5   | 10  | 15  |
| Tyr | Val | Ile | Ala | Ala | Leu | Asn | Leu | Ala | Tyr | Pro | Ile | Ser | Pro | Trp | Lys | 20  | 25  | 30  |     |
| Phe | Lys | Leu | Phe | Cys | Gly | Pro | Pro | Asn | Thr | Thr | Asp | Asp | Ser | Phe | Leu | 35  | 40  | 45  |     |
| Ser | Pro | Ala | Gly | Ala | Pro | Asn | Asn | Ala | Ser | Ala | Leu | Lys | Gly | Ala | Ser | 50  | 55  | 60  |     |
| Glu | Ala | Ile | Val | Glu | Ala | Lys | Phe | Asn | Ser | Ser | Gly | Ile | Tyr | Val | Pro | 65  | 70  | 75  | 80  |
| Glu | Leu | Ser | Lys | Thr | Val | Phe | His | Cys | Cys | Phe | Gly | Asn | Glu | Gln | Gly | 85  | 90  | 95  |     |
| Gln | Asn | Cys | Ser | Ala | Leu | Thr | Asp | Asn | Thr | Glu | Gly | Lys | Thr | Leu | Ala | 100 | 105 | 110 |     |
| Ser | Val | Val | Lys | Ala | Ser | Val | Phe | Arg | Gln | Leu | Gly | Val | Asn | Trp | Asp | 115 | 120 | 125 |     |
| Ile | Glu | Cys | Trp | Met | Lys | Gly | Asp | Leu | Thr | Leu | Phe | Ile | Cys | His | Met | 130 | 135 | 140 |     |
| Glu | Pro | Leu | Pro | Lys | Asn | Pro | Phe | Lys | Asn | Tyr | Asp | Ser | Lys | Val | His | 145 | 150 | 155 | 160 |
| Leu | Leu | Tyr | Asp | Leu | Pro | Glu | Val | Ile | Asp | Asp | Ser | Pro | Leu | Pro | Pro | 165 | 170 | 175 |     |
| Leu | Lys | Asp | Ser | Phe | Gln | Thr | Val | Gln | Cys | Asn | Cys | Ser | Leu | Arg | Gly | 180 | 185 | 190 |     |
| Cys | Glu | Cys | His | Val | Pro | Val | Pro | Arg | Ala | Lys | Leu | Asn | Tyr | Ala | Leu | 195 | 200 | 205 |     |
| Leu | Met | Tyr | Leu | Glu | Ile | Thr | Ser | Ala | Gly | Val | Ser | Phe | Gln | Ser | Pro | 210 | 215 | 220 |     |
| Leu | Met | Ser | Leu | Gln | Pro | Met | Leu | Val | Val | Lys | Pro | Asp | Pro | Pro | Leu | 225 | 230 | 235 | 240 |
| Gly | Leu | His | Met | Glu | Val | Thr | Asp | Asp | Gly | Asn | Leu | Lys | Ile | Ser | Trp | 245 | 250 | 255 |     |
| Asp | Ser | Gln | Thr | Met | Ala | Pro | Phe | Pro | Leu | Gln | Tyr | Gln | Val | Lys | Tyr | 260 | 265 | 270 |     |
| Leu | Glu | Asn | Ser | Thr | Ile | Val | Arg | Glu | Ala | Ala | Glu | Ile | Val | Ser | Ala | 275 | 280 | 285 |     |
| Thr | Ser | Leu | Leu | Val | Asp | Ser | Val | Leu | Pro | Gly | Ser | Ser | Tyr | Glu | Val | 290 | 295 | 300 |     |
| Gln | Val | Arg | Ser | Lys | Arg | Leu | Asp | Gly | Ser | Gly | Val | Trp | Ser | Asp | Trp |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Ser | Pro | Gln | Val | Phe | Thr | Thr | Gln | Asp | Val | Val | Tyr | Phe | Pro | Pro |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Ile | Leu | Thr | Ser | Val | Gly | Ser | Asn | Ala | Ser | Phe | His | Cys | Ile | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Lys | Asn | Glu | Asn | Gln | Ile | Ile | Ser | Ser | Lys | Gln | Ile | Val | Trp | Trp | Arg |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asn | Leu | Ala | Glu | Lys | Ile | Pro | Glu | Ile | Gln | Tyr | Ser | Ile | Val | Ser | Asp |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Arg | Val | Ser | Lys | Val | Thr | Phe | Ser | Asn | Leu | Lys | Ala | Thr | Arg | Pro | Arg |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Gly | Lys | Phe | Thr | Tyr | Asp | Ala | Val | Tyr | Cys | Cys | Asn | Glu | Gln | Ala | Cys |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| His | His | Arg | Tyr | Ala | Glu | Leu | Tyr | Val | Ile | Asp | Val | Asn | Ile | Asn | Ile |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ser | Cys | Glu | Thr | Asp | Gly | Tyr | Leu | Thr | Lys | Met | Thr | Cys | Arg | Trp | Ser |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Pro | Ser | Thr | Ile | Gln | Ser | Leu | Val | Gly | Ser | Thr | Val | Gln | Leu | Arg | Tyr |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| His | Arg | Arg | Ser | Leu | Tyr | Cys | Pro | Asp | Ser | Pro | Ser | Ile | His | Pro | Thr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Glu | Pro | Lys | Asn | Cys | Val | Leu | Gln | Arg | Asp | Gly | Phe | Tyr | Glu | Cys |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Val | Phe | Gln | Pro | Ile | Phe | Leu | Leu | Ser | Gly | Tyr | Thr | Met | Trp | Ile | Arg |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Ile | Asn | His | Ser | Leu | Gly | Ser | Leu | Asp | Ser | Pro | Pro | Thr | Cys | Val | Leu |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Pro | Asp | Ser | Val | Val | Lys | Pro | Leu | Pro | Pro | Ser | Asn | Val | Lys | Ala | Glu |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Ile | Thr | Val | Asn | Thr | Gly | Leu | Leu | Lys | Val | Ser | Trp | Glu | Lys | Pro | Val |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Phe | Pro | Glu | Asn | Asn | Leu | Gln | Phe | Gln | Ile | Arg | Tyr | Gly | Leu | Ser | Gly |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Lys | Glu | Ile | Gln | Trp | Lys | Thr | His | Glu | Val | Phe | Asp | Ala | Lys | Ser | Lys |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Ser | Ala | Ser | Leu | Leu | Val | Ser | Asp | Leu | Cys | Ala | Val | Tyr | Val | Val | Gln |
|     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Val | Arg | Cys | Arg | Arg | Leu | Asp | Gly | Leu | Gly | Tyr | Trp | Ser | Asn | Trp | Ser |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |
| Ser | Pro | Ala | Tyr | Thr | Leu | Val | Met | Asp | Val | Lys | Val | Pro | Met | Arg | Gly |
| 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |
| Pro | Glu | Phe | Trp | Arg | Lys | Met | Asp | Gly | Asp | Val | Thr | Lys | Lys | Glu | Arg |
|     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Val | Thr | Leu | Leu | Trp | Lys | Pro | Leu | Thr | Lys | Asn | Asp | Ser | Leu | Cys | 660 | 665 | 670 |
| Ser | Val | Arg | Arg | Tyr | Val | Val | Lys | His | Arg | Thr | Ala | His | Asn | Gly | Thr | 675 | 680 | 685 |
| Trp | Ser | Glu | Asp | Val | Gly | Asn | Arg | Thr | Asn | Leu | Thr | Phe | Leu | Trp | Thr | 690 | 695 | 700 |
| Glu | Pro | Ala | His | Thr | Val | Thr | Val | Leu | Ala | Val | Asn | Ser | Leu | Gly | Ala | 705 | 710 | 715 |
| Ser | Leu | Val | Asn | Phe | Asn | Leu | Thr | Phe | Ser | Trp | Pro | Met | Ser | Lys | Val | 725 | 730 | 735 |
| Ser | Ala | Val | Glu | Ser | Leu | Ser | Ala | Tyr | Pro | Leu | Ser | Ser | Ser | Cys | Val | 740 | 745 | 750 |
| Ile | Leu | Ser | Trp | Thr | Leu | Ser | Pro | Asp | Asp | Tyr | Ser | Leu | Leu | Tyr | Leu | 755 | 760 | 765 |
| Val | Ile | Glu | Trp | Lys | Ile | Leu | Asn | Glu | Asp | Asp | Gly | Met | Lys | Trp | Leu | 770 | 775 | 780 |
| Arg | Ile | Pro | Ser | Asn | Val | Lys | Lys | Phe | Tyr | Ile | His | Asp | Asn | Phe | Ile | 785 | 790 | 795 |
| Pro | Ile | Glu | Lys | Tyr | Gln | Phe | Ser | Leu | Tyr | Pro | Val | Phe | Met | Glu | Gly | 805 | 810 | 815 |
| Val | Gly | Lys | Pro | Lys | Ile | Ile | Asn | Gly | Phe | Thr | Lys | Asp | Ala | Ile | Asp | 820 | 825 | 830 |
| Lys | Gln | Gln | Asn | Asp | Ala | Gly | Leu | Tyr | Val | Ile | Val | Pro | Ile | Ile | Ile | 835 | 840 | 845 |
| Ser | Ser | Cys | Val | Leu | Leu | Leu | Gly | Thr | Leu | Leu | Ile | Ser | His | Gln | Arg | 850 | 855 | 860 |
| Met | Lys | Lys | Leu | Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | Asn | Cys | Ser | 865 | 870 | 875 |
| Trp | Ala | Gln | Gly | Leu | Asn | Phe | Gln | Lys | Asp | Ile | Ser | Leu | His | Glu | Val | 885 | 890 | 895 |
| Phe | Ile | Phe | Arg |     |     |     |     |     |     |     |     |     |     |     |     | 900 |     |     |

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2461 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: A20 (OB-Re)



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| GAGGAATCGT | TCTGCAAATC | CAGGTGTACA  | CCTCTGAAGA | AAGATGATGT  | GTCAGAAATT | 60   |
| CTATGTGGTT | TTGTTACACT | GGGAATTTCT  | TTATGTGATA | GCTGCACTTA  | ACCTGGCATA | 120  |
| TCCAATCTCT | CCCTGGAAAT | TTAAGTTGTT  | TTGTGGACCA | CCGAACACAA  | CCGATGACTC | 180  |
| CTTTCTCTCA | CCTGCTGGAG | CCCCAAACAA  | TGCCTCGGCT | TTGAAGGGGG  | CTTCTGAAGC | 240  |
| AATTGTTGAA | GCTAAATTTA | ATTCAAGTGG  | TATCTACGTT | CCTGAGTTAT  | CCAAAACAGT | 300  |
| CTTCCACTGT | TGCTTTGGGA | ATGAGCAAGG  | TCAAACTGTC | TCTGCACTCA  | CAGACAACAC | 360  |
| TGAAGGGAAG | ACACTGGCTT | CAGTAGTGAA  | GGCTTCAGTT | TTTCGCCAGC  | TAGGTGTAAA | 420  |
| CTGGGACATA | GAGTGCTGGA | TGAAAGGGGA  | CTTGACATTA | TTCATCTGTC  | ATATGGAGCC | 480  |
| ATTACCTAAG | AACCCCTTCA | AGAATTATGA  | CTCTAAGGTC | CATCTTTTAT  | ATGATCTGCC | 540  |
| TGAAGTCATA | GATGATTCGC | CTCTGCCCCC  | ACTGAAAGAC | AGCTTTTCAGA | CTGTCCAATG | 600  |
| CAACTGCAGT | CTTCGGGGAT | GTGAATGTCA  | TGTGCCGGTA | CCCAGAGCCA  | AACTCAACTA | 660  |
| CGCTCTTCTG | ATGTATTTGG | AAATCACATC  | TGCCGGTGTG | AGTTTTTCAGT | CACCTCTGAT | 720  |
| GTCAGTGCAG | CCCATGCTTG | TTGTGAAACC  | CGATCCACCC | TTAGGTTTGC  | ATATGGAAGT | 780  |
| CACAGATGAT | GGTAATTTAA | AGATTTCTTG  | GGACAGCCAA | ACAATGGCAC  | CATTTCCGCT | 840  |
| TCAATATCAG | GTGAAATATT | TAGAGAATTC  | TACAATTGTA | AGAGAGGCTG  | CTGAAATTGT | 900  |
| CTCAGCTACA | TCTCTGCTGG | TAGACAGTGT  | GCTTCCTGGA | TCTTCATATG  | AGGTCCAGGT | 960  |
| GAGGAGCAAG | AGACTGGATG | GTTTCAGGAGT | CTGGAGTGAC | TGGAGTTCAC  | CTCAAGTCTT | 1020 |
| TACCACACAA | GATGTTGTGT | ATTTTCCACC  | CAAAATTCTG | ACTAGTGTTG  | GATCGAATGC | 1080 |
| TTCTTTTCAT | TGCATCTACA | AAAACGAAAA  | CCAGATTATC | TCCTCAAAAC  | AGATAGTTTG | 1140 |
| GTGGAGGAAT | CTAGCTGAGA | AAATCCCTGA  | GATACAGTAC | AGCATTGTGA  | GTGACCGAGT | 1200 |
| TAGCAAAGTT | ACCTTCTCCA | ACCTGAAAGC  | CACCAGACCT | CGAGGGAAGT  | TTACCTATGA | 1260 |
| CGCAGTGTAC | TGCTGCAATG | AGCAGGCGTG  | CCATCACCGC | TATGCTGAAT  | TATACGTGAT | 1320 |
| CGATGTCAAT | ATCAATATAT | CATGTGAAAC  | TGACGGGTAC | TTAACTAAAA  | TGACTTGCAG | 1380 |
| ATGGTCACCC | AGCACAATCC | AATCACTAGT  | GGGAAGCACT | GTGCAGCTGA  | GGTATCACAG | 1440 |
| GCGCAGCCTG | TATTGTCCTG | ATAGTCCATC  | TATTCATCCT | ACGTCTGAGC  | CCAAAACTG  | 1500 |
| CGTCTTACAG | AGAGACGGCT | TTTATGAATG  | TGTTTTCCAG | CCAATCTTTC  | TATTATCTGG | 1560 |
| CTATACAATG | TGGATCAGGA | TCAACCATTG  | TTTAGGTTCA | CTTGACTCGC  | CACCAACGTG | 1620 |
| TGTCCTTCCT | GACTCCGTAG | TAAAACCACT  | ACCTCCATCT | AACGTAAAAG  | CAGAGATTAC | 1680 |
| TGTAAACACT | GGATTATTGA | AAGTATCTTG  | GGAAAAGCCA | GTCTTTCCGG  | AGAATAACCT | 1740 |
| TCAATTCCAG | ATTCGATATG | GCTTAAGTGG  | AAAAGAAATA | CAATGGAAGA  | CACATGAGGT | 1800 |
| ATTCGATGCA | AAGTCAAAGT | CTGCCAGCCT  | GCTGGTGTCA | GACCTCTGTG  | CAGTCTATGT | 1860 |

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GGTCCAGGTT CGCTGCCGGC GGTGGATGG ACTAGGATAT TGGAGTAATT GGAGCAGTCC 1920
AGCCTATACG CTTGTCATGG ATGTAAAAGT TCCTATGAGA GGGCCTGAAT TTTGGAGAAA 1980
AATGGATGGG GACGTTACTA AAAAGGAGAG AAATGTCACC TTGCTTTGGA AGCCCCTGAC 2040
GAAAAATGAC TCACTGTGTA GTGTGAGGAG GTACGTGGTG AAGCATCGTA CTGCCCACAA 2100
TGGGACGTGG TCAGAAGATG TGGGAAATCG GACCAATCTC ACTTTCCTGT GGACAGAACC 2160
AGCGCACACT GTTACAGTTC TGGCTGTCAA TTCCCTCGGC GCTTCCCTTG TGAATTTTAA 2220
CCTTACCTTC TCATGGCCCA TGAGTAAAGT GAGTGCTGTG GAGTCACTCA GTGCTTATCC 2280
CCTGAGCAGC AGCTGTGTCA TCCTTTCCTG GAACTGTGCA CCTGATGATT ATAGTCTGTT 2340
ATATCTGGTT ATTGAATGGA AGATCCTTAA TGAAGATGAT GGAATGAAGT GGCTTAGAAT 2400
TCCCTCGAAT GTTAAAAAGT TTTATATCCA CGGTATGTGT ACTGTACTTT TCATGGATTA 2460
G 2461

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## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Re

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
 1 5 10 15
Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
 20 25 30
Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
 35 40 45
Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
 50 55 60
Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65 70 75 80
Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
 85 90 95
Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
 100 105 110

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ser | Val | Val | Lys | Ala | Ser | Val | Phe | Arg | Gln | Leu | Gly | Val | Asn | Trp | Asp |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Ile | Glu | Cys | Trp | Met | Lys | Gly | Asp | Leu | Thr | Leu | Phe | Ile | Cys | His | Met |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Glu | Pro | Leu | Pro | Lys | Asn | Pro | Phe | Lys | Asn | Tyr | Asp | Ser | Lys | Val | His |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Leu | Leu | Tyr | Asp | Leu | Pro | Glu | Val | Ile | Asp | Asp | Ser | Pro | Leu | Pro | Pro |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Leu | Lys | Asp | Ser | Phe | Gln | Thr | Val | Gln | Cys | Asn | Cys | Ser | Leu | Arg | Gly |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Cys | Glu | Cys | His | Val | Pro | Val | Pro | Arg | Ala | Lys | Leu | Asn | Tyr | Ala | Leu |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Leu | Met | Tyr | Leu | Glu | Ile | Thr | Ser | Ala | Gly | Val | Ser | Phe | Gln | Ser | Pro |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Leu | Met | Ser | Leu | Gln | Pro | Met | Leu | Val | Val | Lys | Pro | Asp | Pro | Pro | Leu |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Gly | Leu | His | Met | Glu | Val | Thr | Asp | Asp | Gly | Asn | Leu | Lys | Ile | Ser | Trp |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Asp | Ser | Gln | Thr | Met | Ala | Pro | Phe | Pro | Leu | Gln | Tyr | Gln | Val | Lys | Tyr |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Leu | Glu | Asn | Ser | Thr | Ile | Val | Arg | Glu | Ala | Ala | Glu | Ile | Val | Ser | Ala |  |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Thr | Ser | Leu | Leu | Val | Asp | Ser | Val | Leu | Pro | Gly | Ser | Ser | Tyr | Glu | Val |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |
| Gln | Val | Arg | Ser | Lys | Arg | Leu | Asp | Gly | Ser | Gly | Val | Trp | Ser | Asp | Trp |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |
| Ser | Ser | Pro | Gln | Val | Phe | Thr | Thr | Gln | Asp | Val | Val | Tyr | Phe | Pro | Pro |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |
| Lys | Ile | Leu | Thr | Ser | Val | Gly | Ser | Asn | Ala | Ser | Phe | His | Cys | Ile | Tyr |  |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |  |
| Lys | Asn | Glu | Asn | Gln | Ile | Ile | Ser | Ser | Lys | Gln | Ile | Val | Trp | Trp | Arg |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |
| Asn | Leu | Ala | Glu | Lys | Ile | Pro | Glu | Ile | Gln | Tyr | Ser | Ile | Val | Ser | Asp |  |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |
| Arg | Val | Ser | Lys | Val | Thr | Phe | Ser | Asn | Leu | Lys | Ala | Thr | Arg | Pro | Arg |  |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |
| Gly | Lys | Phe | Thr | Tyr | Asp | Ala | Val | Tyr | Cys | Cys | Asn | Glu | Gln | Ala | Cys |  |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |
| His | His | Arg | Tyr | Ala | Glu | Leu | Tyr | Val | Ile | Asp | Val | Asn | Ile | Asn | Ile |  |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |  |
| Ser | Cys | Glu | Thr | Asp | Gly | Tyr | Leu | Thr | Lys | Met | Thr | Cys | Arg | Trp | Ser |  |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |
| Pro | Ser | Thr | Ile | Gln | Ser | Leu | Val | Gly | Ser | Thr | Val | Gln | Leu | Arg | Tyr |  |  |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |

[illegible]

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: OB-Ra
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
 

|     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Gln | Lys | Arg | Thr | Asp | Leu |
| 1   |     |     |     |     | 5   |     |     |

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 276 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: OB-Rb
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
 

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Gln | Lys | Pro | Glu | Thr | Phe | Glu | Gln | Leu | Phe | Thr | Lys | His | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ser | Val | Ile | Phe | Gly | Pro | Leu | Leu | Leu | Glu | Pro | Glu | Pro | Ile | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Ile | Ser | Val | Asp | Thr | Ala | Trp | Lys | Asn | Lys | Asp | Glu | Met | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ala | Ala | Met | Val | Ser | Leu | Leu | Trp | Thr | Thr | Pro | Asp | Pro | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Ile | Cys | Ile | Ser | Asp | Gln | Cys | Asn | Ser | Ala | Asn | Phe | Ser | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro Ser  
 85 90 95  
 Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr Asp  
 100 105 110  
 Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser Ser  
 115 120 125  
 Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Ser Trp Glu Thr  
 130 135 140  
 Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Glu Gln Pro Thr Met Ile  
 145 150 155 160  
 Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu Glu  
 165 170 175  
 Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr Leu  
 180 185 190  
 Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly  
 195 200 205  
 Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp  
 210 215 220  
 Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu  
 225 230 235 240  
 Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln Phe  
 245 250 255  
 Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys  
 260 265 270  
 Asp Phe Thr Val  
 275

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: OB-Rc
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
 

Asn Phe Gln Lys Val Thr Val  
 1 5

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: OB-Rd
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Gln | Lys | Asp | Ile | Ser | His | Glu | Val | Phe | Ile | Phe | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: OB-Re
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Tyr | Ile | His | Gly | Met | Cys | Thr | Val | Leu | Phe | Met | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

(2) INFORMATION FOR SEQ ID NO:19:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Leu | Pro | Lys | Asn | Pro | Phe | Lys | Asn | Tyr | Asp | Ser | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Arg | Arg | Ser | Leu | Tyr | Cys | Pro | Asp | Ser | Pro | Ser | Ile | His | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Pro | Lys |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

|             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln         | Arg | Met | Lys | Lys | Leu | Phe | Trp | Asp | Asp | Val | Pro | Asn | Pro | Lys | Asn |
| 1           |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys Ser Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 166 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| AGGGNAAGCG | CCGAGGGAAT | TGACAGCCAG | AACTGTAACA | GTGTGCGCTG | GTTCTGTCCA | 60  |
| CAGGAAAGTG | AGATTGGTCC | GATTTCCCAC | ATCTTCTGAC | CACGTCCCAT | TGTGGGCAGT | 120 |
| ACGATGCTTC | ACCACGTACC | TCCTCACACT | ACACAGTGAG | TCATTT     |            | 166 |

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 320 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA | 60  |
| TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCT  | 120 |
| CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC | 180 |
| TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT | 240 |
| GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA | 300 |
| TGATGGAATG AAGTGGCTTA                                             | 320 |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GATTACTGGA GATGCAGTTG GTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT | 60  |
| CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTTGT CTCTGACACT | 120 |
| CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG                         | 158 |

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 46

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTGAGGCTC TGTGTTTCATT TGATGTTTCAG 60
AAGTCAGCAA GGTTCCTCATA TGTCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG 120
CTAACAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACTACTTG GTGTTTTACT 180
TAAAGATACG AG 192

```

## (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 168 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: 58

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

AGACTGACAA GGAAGTTTTTC TCATCTAACA AGCAAGCAAA GGAAGTGCTT ATGTNCTGTG 60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT 120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA
168

```

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 259 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: S3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

AGAATTATGA CTCTAAGGTC CATGTTTTAT ATGATCTGCC TGAAGTCATA GATGATTCGC 60

```



CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTCGGGGAT 120  
 GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTGG 180  
 NAATCACATC TGCCGGTGTG AGTTTTTCAGT CACCTCTGAT GTCAGTGCAG CCCATGCTTG 240  
 TTGTGAAACC CGATCCACC 259

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 

- (B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG 60  
 GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACTTA AATTTCCAGG 120  
 GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA 180  
 AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTCAG 240  
 AACGATTCTT 250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC 18

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG

22

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTTCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTTCGTACCC GACGTCACTG

20